

OIPE

RAW SEQUENCE LISTING

DATE: 06/25/2001

PATENT APPLICATION: US/09/424,487B

TIME: 11:59:11

Input Set : A:\71278264.app

Output Set: N:\CRF3\06252001\I424487B.raw

ENTERED

3 <110> APPLICANT: CHOO, YEN
4 KLUG, AARON
5 ISALAN, MARK
7 <120> TITLE OF INVENTION: NUCLEIC ACID BINDING PROTEINS
9 <130> FILE REFERENCE: 71278/264975
11 <140> CURRENT APPLICATION NUMBER: 09/424,487B
C--> 12 <141> **CURRENT FILING DATE: 2000-02-29**
14 <150> PRIOR APPLICATION NUMBER: GB 9710809.6
15 <151> PRIOR FILING DATE: 1997-05-23
17 <150> PRIOR APPLICATION NUMBER: PCT/GB98/01512
18 <151> PRIOR FILING DATE: 1998-05-26
20 <160> NUMBER OF SEQ ID NOS: 114
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 264
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(264)
33 <220> FEATURE:
34 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
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37 gca gaa gag aag cct ttt cag tgt cga atc tgc atg cgt aac ttc agc 48
38 Ala Glu Glu Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser
39 1 5 10 15
41 gat cgt act act ctt acc cgc cac acg agg acc cac aca ggc gag aag 96
42 Asp Arg Thr Thr Leu Thr Arg His Thr Arg Thr His Thr Gly Glu Lys
43 20 25 30
45 cct ttt cag tgt cga atc tgc atg cgt aac ttc agc agg agc gat aac 144
46 Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp Asn
47 35 40 45
49 ctt acg aga cac cta agg acc cac aca ggc gag aag cct ttt cag tgt 192
50 Leu Thr Arg His Leu Arg Thr His Thr Gly Glu Lys Pro Phe Gln Cys
51 50 55 60
53 cga atc tgc atg cgt aac ttc agg caa gct gat cat ctt caa gag cac 240
54 Arg Ile Cys Met Arg Asn Phe Arg Gln Ala Asp His Leu Gln Glu His
55 65 70 75 80
57 cta aag acc cac aca ggc gag aag 264
58 Leu Lys Thr His Thr Gly Glu Lys
59 85
62 <210> SEQ ID NO: 2
63 <211> LENGTH: 88
64 <212> TYPE: PRT
65 <213> ORGANISM: Artificial Sequence
67 <220> FEATURE:
68 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic amino acid

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70 <400> SEQUENCE: 2

71 Ala Glu Glu Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser

72 1 5 10 15

74 Asp Arg Thr Thr Leu Thr Arg His Thr Arg Thr His Thr Gly Glu Lys

75 20 25 30

77 Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp Asn

78 35 40 45

80 Leu Thr Arg His Leu Arg Thr His Thr Gly Glu Lys Pro Phe Gln Cys

81 50 55 60

83 Arg Ile Cys Met Arg Asn Phe Arg Gln Ala Asp His Leu Gln Glu His

84 65 70 75 80

86 Leu Lys Thr His Thr Gly Glu Lys

87 85

90 <210> SEQ ID NO: 3

91 <211> LENGTH: 24

92 <212> TYPE: PRT

93 <213> ORGANISM: Artificial Sequence

95 <220> FEATURE:

96 <223> OTHER INFORMATION: Description of Artificial Sequence: Zinc finger

97 motif

99 <220> FEATURE:

100 <221> NAME/KEY: MOD_RES

101 <222> LOCATION: (1)

102 <223> OTHER INFORMATION: Any amino acid

104 <220> FEATURE:

105 <221> NAME/KEY: MOD_RES

106 <222> LOCATION: (3)..(6)

107 <223> OTHER INFORMATION: This region may encompass 2-4 residues consisting of

108 any amino acid

110 <220> FEATURE:

111 <221> NAME/KEY: MOD_RES

112 <222> LOCATION: (8)..(10)

113 <223> OTHER INFORMATION: This region may encompass 2-3 residues consisting of

114 any amino acid

116 <220> FEATURE:

117 <221> NAME/KEY: MOD_RES

118 <222> LOCATION: (12)..(16)

119 <223> OTHER INFORMATION: Any amino acid

121 <220> FEATURE:

122 <221> NAME/KEY: MOD_RES

123 <222> LOCATION: (18)..(19)

124 <223> OTHER INFORMATION: Any amino acid

126 <220> FEATURE:

127 <221> NAME/KEY: MOD_RES

128 <222> LOCATION: (21)..(23)

129 <223> OTHER INFORMATION: Any amino acid

131 <400> SEQUENCE: 3

W--> 132 Xaa Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa

133 1 5 10 15

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      136                20
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      142 <213> ORGANISM: Artificial Sequence
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      145 <223> OTHER INFORMATION: Description of Artificial Sequence: Linker
      147 <400> SEQUENCE: 4
      148 Thr Gly Glu Lys
      149 1
      152 <210> SEQ ID NO: 5
      153 <211> LENGTH: 5
      154 <212> TYPE: PRT
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      157 <220> FEATURE:
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      162 1 5
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      168 <213> ORGANISM: Artificial Sequence
      170 <220> FEATURE:
      171 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
      172 structure
      174 <400> SEQUENCE: 6
      175 Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln Lys Ser Asp
      176 1 5 10 15
      178 Leu Val Lys His Gln Arg Thr His Thr Gly
      179 20 25
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      184 <212> TYPE: PRT
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      187 <220> FEATURE:
      188 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
      189 structure
      191 <400> SEQUENCE: 7
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      193 1 5 10 15
      195 Leu Thr Arg His Gln Arg Ile His Thr Gly Glu Lys Pro
      196 20 25
      199 <210> SEQ ID NO: 8
      200 <211> LENGTH: 6
      201 <212> TYPE: PRT
      202 <213> ORGANISM: Artificial Sequence
      204 <220> FEATURE:

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Input Set : A:\71278264.app

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205 <223> OTHER INFORMATION: Description of Artificial Sequence: Leader peptide
 207 <400> SEQUENCE: 8
 208 Met Ala Glu Glu Lys Pro
 209 1 5
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 217 <220> FEATURE:
 218 <223> OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
 219 peptide
 221 <400> SEQUENCE: 9
 222 Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Asp Arg Ser Ser Leu
 223 1 5 10 15
 225 Thr Arg His Thr Arg Thr His Thr Gly Glu Lys Pro
 226 20 25
 229 <210> SEQ ID NO: 10
 230 <211> LENGTH: 28
 231 <212> TYPE: PRT
 232 <213> ORGANISM: Artificial Sequence
 234 <220> FEATURE:
 235 <223> OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
 236 peptide
 238 <400> SEQUENCE: 10
 239 Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Asp Arg Ser His Leu
 240 1 5 10 15
 242 Thr Arg His Thr Arg Thr His Thr Gly Glu Lys Pro
 243 20 25
 246 <210> SEQ ID NO: 11
 247 <211> LENGTH: 27
 248 <212> TYPE: PRT
 249 <213> ORGANISM: Artificial Sequence
 251 <220> FEATURE:
 252 <223> OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
 253 peptide
 255 <400> SEQUENCE: 11
 256 Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Asp Arg Ser Asn Leu
 257 1 5 10 15
 259 Thr Arg His Thr Arg Thr His Thr Gly Glu Lys
 260 20 25
 263 <210> SEQ ID NO: 12
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 265 <212> TYPE: PRT
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 269 <223> OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
 270 peptide
 272 <400> SEQUENCE: 12
 273 Met Ala Glu Glu Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg

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274      1              5              10              15
276 Arg Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr
277              20              25              30
279 Gly Gln Lys Pro
280              35
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284 <211> LENGTH: 27
285 <212> TYPE: PRT
286 <213> ORGANISM: Artificial Sequence
288 <220> FEATURE:
289 <223> OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
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292 <400> SEQUENCE: 13
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294      1              5              10              15
296 Thr His Ile Arg Thr His Thr Gly Glu Lys Pro
297              20              25
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301 <211> LENGTH: 26
302 <212> TYPE: PRT
303 <213> ORGANISM: Artificial Sequence
305 <220> FEATURE:
306 <223> OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
307      peptide
309 <400> SEQUENCE: 14
310 Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Ser Asp Arg Lys Arg
311      1              5              10              15
313 His Thr Lys Ile His Leu Arg Gln Lys Asp
314              20              25
317 <210> SEQ ID NO: 15
318 <211> LENGTH: 4
319 <212> TYPE: PRT
320 <213> ORGANISM: Artificial Sequence
322 <220> FEATURE:
323 <223> OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
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326 <400> SEQUENCE: 15
327 Arg Leu Glu Tyr
328      1
331 <210> SEQ ID NO: 16
332 <211> LENGTH: 4
333 <212> TYPE: PRT
334 <213> ORGANISM: Artificial Sequence
336 <220> FEATURE:
337 <223> OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
338      peptide
340 <400> SEQUENCE: 16
341 Arg Ser Glu Asp
342      1

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VERIFICATION SUMMARY

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Input Set : A:\71278264.app

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:135 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3